Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/051,843 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos ·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ____ · Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/051,843B   TIME: 10:36:01

Input Set : A:\SEQUENCE.asc
Output Set: N:\CRF3\07052001\I051843B.raw

Does Not Comply Corrected Diskette Needed   *See pages*

```
 4 <110> APPLICANT: Willson, Tracy
 5        Nicola, Nicos A.
 6        Hilton, Douglas J.
 7        Metcalf, Donald
 8        Zhang, Jian G.
10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
11        ENCODING SAME
13 <130> FILE REFERENCE: Davies cc
15 <140> CURRENT APPLICATION NUMBER: 09/051,843B
16 <141> CURRENT FILING DATE: 2001-06-20
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1383
24 <212> TYPE: DNA
25 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (61)..(1338)
31 <220> FEATURE:
32 <221> NAME/KEY: unsure
33 <222> LOCATION: (121)
34 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
35        region
37 <220> FEATURE:
38 <221> NAME/KEY: unsure
39 <222> LOCATION: (122)
40 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
41        region
43 <220> FEATURE:
44 <221> NAME/KEY: unsure
45 <222> LOCATION: (123)
46 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
47        region
49 <220> FEATURE:
50 <221> NAME/KEY: unsure
51 <222> LOCATION: (640)
52 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
53        region
55 <220> FEATURE:
56 <221> NAME/KEY: unsure
57 <222> LOCATION: (641)
58 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
59        region
61 <220> FEATURE:
62 <221> NAME/KEY: unsure
63 <222> LOCATION: (642)
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C--> 16 <141> CURRENT FILING DATE: 2001-06-20

see Item #10 on the ERROR SUMMARY sheet

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                        RAW SEQUENCE LISTING          DATE: 07/05/2001
                        PATENT APPLICATION:  US/09/051,843B    TIME: 10:36:01

                        Input Set : A:\SEQUENCE.asc
                        Output Set: N:\CRF3\07052001\I051843B.raw

        64 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
        65      region
        67 <400> SEQUENCE: 1
        68 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60
        71 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg    108
        72 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
        73  1               5                  10                  15
W-->    75 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca    156
W-->    76 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
        77              20                  25                  30
        79 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata    204
        80 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
        81          35                  40                  45
        83 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga    252
        84 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
        85      50                  55                  60
        87 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa    300
        88 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
        89 65                  70                  75                  80
        91 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag    348
        92 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
        93              85                  90                  95
        95 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg    396
        96 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
        97              100                 105                 110
        99 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg    444
        100 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
        101          115                 120                 125
        103 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc   492
        104 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
        105          130                 135                 140
        107 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac   540
        108 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
        109 145                 150                 155                 160
        111 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat   588
        112 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
        113              165                 170                 175
        115 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa   636
        116 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
        117              180                 185                 190
W-->    119 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat   684
W-->    120 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
        121          195                 200                 205
        123 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat   732
        124 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
        125          210                 215                 220
        127 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt   780
        128 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
        129 225                 230                 235                 240
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131 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc    828
132 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
133             245                 250                 255
135 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat    876
136 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
137             260                 265                 270
139 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga    924
140 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
141         275                 280                 285
143 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac    972
144 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
145     290                 295                 300
147 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt   1020
148 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
149 305                 310                 315                 320
151 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt   1068
152 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
153             325                 330                 335
155 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca   1116
156 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
157             340                 345                 350
159 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg   1164
160 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
161             355                 360                 365
163 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt   1212
164 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
165     370                 375                 380
167 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag   1260
168 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
169 385                 390                 395                 400
171 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg   1308
172 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
173             405                 410                 415
175 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc   1358
176 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
177             420                 425
179 tttcttgcct tcaatgtgac cctgt                                      1383
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 426
185 <212> TYPE: PRT
186 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
188 <220> FEATURE:
189 <221> NAME/KEY: unsure
190 <222> LOCATION: (21)
191 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
193 <220> FEATURE:
194 <221> NAME/KEY: unsure
195 <222> LOCATION: (194)
196 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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see page 1

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/051,843B   TIME: 10:36:01

Input Set : A:\SEQUENCE.asc
Output Set: N:\CRF3\07052001\I051843B.raw

```
198 <400> SEQUENCE: 2
199 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
200  1               5               10               15
W--> 202 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
203               20               25               30
205 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
206           35               40               45
208 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
209      50               55               60
211 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
212  65               70               75               80
214 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
215               85               90               95
217 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
218           100              105              110
220 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
221           115              120              125
223 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
224      130              135              140
226 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
227 145              150              155              160
229 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
230               165              170              175
232 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
233               180              185              190
W--> 235 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
236           195              200              205
238 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
239           210              215              220
241 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
242 225              230              235              240
244 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
245               245              250              255
247 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
248               260              265              270
250 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
251           275              280              285
253 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
254      290              295              300
256 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
257 305              310              315              320
259 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
260               325              330              335
262 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
263           340              345              350
265 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
266           355              360              365
268 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
269      370              375              380
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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/051,843B   TIME: 10:36:01

Input Set : A:\SEQUENCE.asc
Output Set: N:\CRF3\07052001\I051843B.raw

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271 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
272 385             390             395             400
274 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
275             405             410             415
277 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
278             420             425
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 1383
283 <212> TYPE: DNA
284 <213> ORGANISM: Human IL-13 receptor alpha-chain         — see page 1
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
290 <400> SEQUENCE: 3
291 gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggc gagaggctgc 60
294 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc    108
295 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
296  1           5               10                  15
298 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca    156
299 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
300             20              25                  30
302 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata    204
303 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
304             35              40                  45
306 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg    252
307 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
308         50              55              60
310 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa    300
311 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
312 65              70              75                  80
314 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa    348
315 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
316                 85              90                  95
318 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg    396
319 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
320             100         .       105             110
322 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg    444
323 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
324         115             120             125
326 act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct    492
327 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
328     130             135             140
330 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac    540
331 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
332 145             150             155             160
334 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt    588
335 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
336             165             170             175
338 aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag    636
```

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a c rresponding explanation is presented in the <220> to
<223> fields f each sequence which presents at least one n r Xaa.

VERIFICATION SUMMARY   DATE: 07/05/2001
PATENT APPLICATION: **US/09/051,843B**   TIME: 10:36:02

Input Set : **A:\SEQUENCE.asc**
Output Set: **N:\CRF3\07052001\I051843B.raw**

```
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
```